

Investigator Fancy, Chen

Date \_\_\_\_\_

Subject Final Assembling of UCP<sub>2</sub> DNA SequenceFiled in Book Number/Title Full length cDNA Retrieving

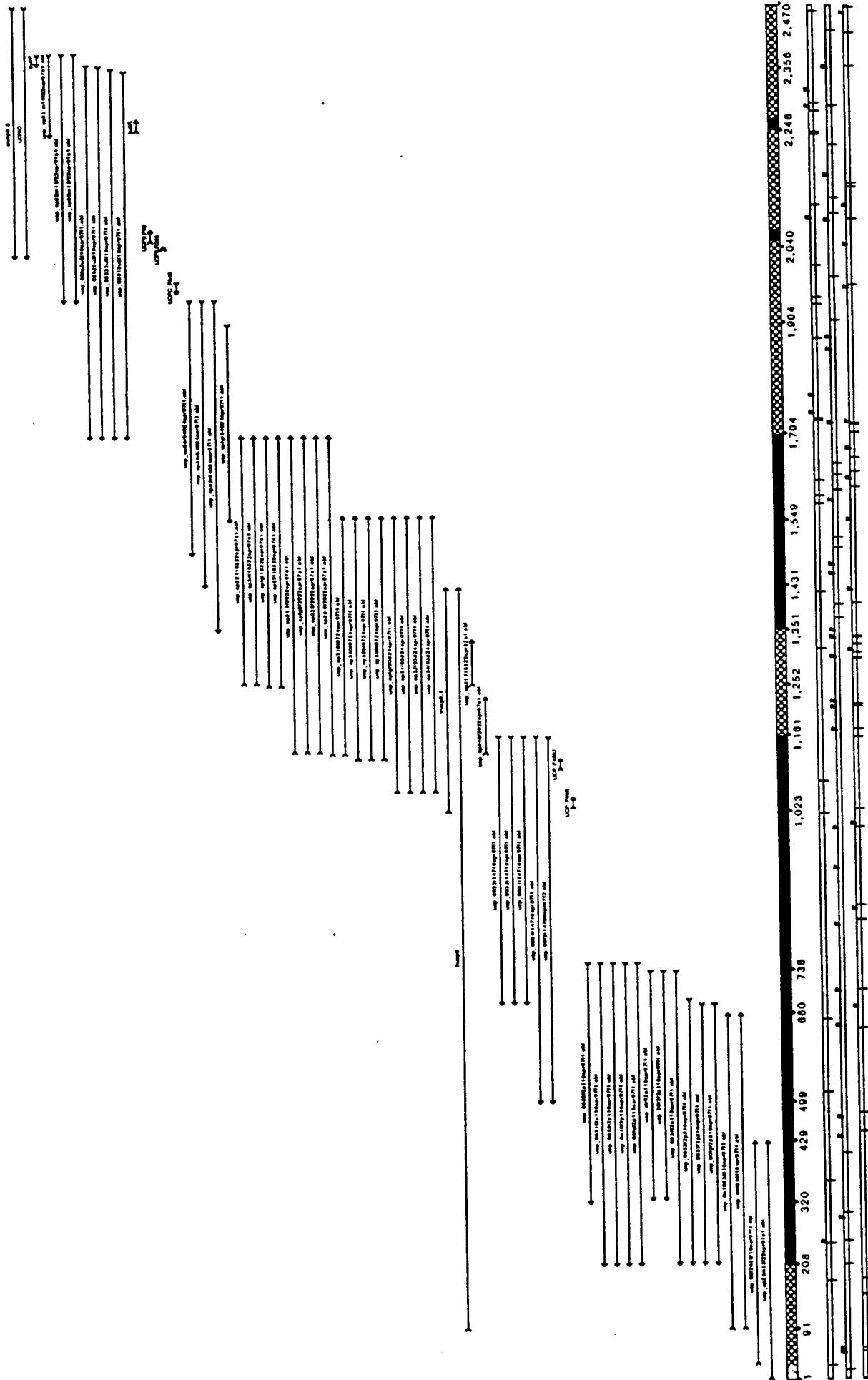
More sequence results were obtained from Sequence core facility. After a thorough editing, all the DNA fragments assembled and contained one open reading frame coding for a protein with 58% identity to UCP1 and 73% to UCP2.  
(See attached documents.)

Countersigned by \_\_\_\_\_

L. Ma

Date \_\_\_\_\_

Contig. J49  
Sequencer "nucr-test"



for 9173

Page 1 of 2

Lili Ms

EXHIBIT A p.2 of 4 09/08/97

P-14

CompCheck: 1254

Gap Weight: 3.000      Average Match: 0.540  
 Length Weight: 0.100      Average Mismatch: -0.396

Quality: 315.9      Length: 311  
 Ratio: 1.032      Gaps: 2  
 Percent Similarity: 75.817      Percent Identity: 58.170

ucp3.pep x UCP1



for P173

1 MVGLKPSDVPPPTMAVKFLGAGTAACFADLVTPLDTAKVRLQIQGENQAV 50  
 |.|||.:||||.|||:|.:|||:||||:||||:||||:||||:||||:||||:  
 1 MGGLTASDVHPTLGVQLFSAGIAACLAADVITPLDTAKVRLQVQGE...C 47

51 QTARLVQYRGVLGTLTMVRTEGPCSPYNGLVAQGLQRQMSFASIRIGLYD 100  
 .|.:|||:|||||. .|:|||. .|.|.|||:|||:|||:  
 48 PTSSVIRYKGVLGTITAVVKTEGRMKLYSGLPAGLQRQISSASLRIGLYD 97

101 SVKVQVTPKGADNSSLTTRILAGCTTGAMAVTCAQPTDVVKVRFOASIHL 150  
 .|.:|||: .|...|||:|||:|||:|||:|||:|||:|||:  
 98 TVQEFLTAGKETAPSLGSKILAGLTTGGAVFIGQPTEVVVKVRLQAQSHL 147

151 GPSRSDRKYSgtMDAYRTIAREEGVRLWKGLPNIMRNAIVNCAEVVTY 200  
 .|.. :|.| :|||.|| .||: ||||| |||:|||.||:|||:  
 148 HGIKP..RYTGTYNAYRIIATTEGLTGLWKGTTPNLMRSVIINCTELVTY 195

201 DILKEKLLDYHLLTDNFPCHFVSAFGAGFCATVVASPVDVVKTRYMNSPP 250  
 |::|| .| .:|||.||:|||: ||||| .:|||:|||:|||:  
 196 DLMKEAFVKNNILADDVPCHLVSALIAGFCATAMSSPVDVVKTRFINSPP 245

251 GQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFVTYEQLKRA 300  
 ||| .| .:|||.|||:|||: .|||:|||:|||:  
 246 GQYKSVPNCAMKVFTNEGPTAFFKGLVPSFLRLGSWNVIMFVCFEQLKRE 295

301 LMKVQMLRESP 311  
 | | . .:::  
 296 LSKSRQTMDC 306

Ji:Ms

CompCheck: 1254

Gap Weight: 3.000      Average Match: 0.540  
 Length Weight: 0.100      Average Mismatch: -0.396

Quality: 362.4      Length: 313  
 Ratio: 1.173      Gaps: 3

Percent Similarity: 85.065      Percent Identity: 73.377

ucp3.pep x UCP2



P173  
JUL 2 1999

1 MVGLKPSDVPPPTMAVKFLGAGTAACFADLVTPLDTAKVRLQIQGENQA. 49  
 ||||:|.:||||| .|||||||||:||||:|||||||||:||:  
 1 MVGFKATDVPPTATVKFLGAGTAACIADLITPLDTAKVRLQIQGESQGP 50

50 VQTARLVQYRGVLGTILTMVRTEGPCSPYNGLVAGLQRQMSFASIRIGLY 99  
 |... .|||||:||||| .||| .||| .||| .||| .||| .|||:  
 51 VRATASAQYRGVMGTILTMVRTEGPRSLYNGLVAGLQRQMSFASVRIGLY 100

100 DSVKQVYTPKGADNSSLTTRILAGCTTGAMAVTCAQPTDVVKVRFQASI 149  
 |||||.|| .|| .:|| .|| .:|| .|| .:|| .|| .:|| .||:  
 101 DSVKQFYT.KGSEHASIGSRLLAGSTTGALAVAVAQPTDVVKVRFQAQAR 149

150 LGPSRSDRKYSGTMDAYRTIAREEGVRGLWKGTLPNIMRNAIVNCAEVVT 199  
 | . :|| . :|| .:|| .|| .:|| .|| .:|| .|| .:||:  
 150 AG...GGRRYQSTVNAYKTIAREEGFRGLWKGTPNVARNAIVNCAELVT 196

200 YDILKEKLLDYHLLTDNFPCFVSAFGAGFCATVVASPVDVVKTRYMNSP 249  
 || .:|| . :|| .:|| .|| .:|| .|| .:|| .|| .:||:  
 197 YDLIKDALLKANLMTDDLPCHFISAFGAGFCTTVIASPVDVVKTRYMNSA 246

250 PGQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFVTYEQLKR 299  
 |||| .: .|| .: .|| .|| .:|| .|| .:|| .|| .:||:  
 247 LGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKR 296

300 ALMKVQMLRESPF 312  
 ||| . .|| .||:  
 297 ALMAACTSREAPPF 309

JUL 2 1999